# Upgrade of the Cellular General Purpose Monte Carlo Tool FOAM to version 2.06

#### S. Jadach

Institute of Nuclear Physics, Academy of Sciences, ul. Radzikowskiego 152, 31-342 Cracow, Poland, and CERN Department of Physics, Theory Division CH-1211 Geneva 23, Switzerland

and

#### P. Sawicki

Institute of Nuclear Physics, Academy of Sciences, ul. Radzikowskiego 152, 31-342 Cracow, Poland

#### Abstract

FOAM-2.06 is an upgraded version of FOAM, a general purpose, self-adapting Monte Carlo event generator. In comparison with FOAM-2.05, it has two important improvements. New interface to random numbers lets the user to choose from the three "state of the art" random number generators. Improved algorithms for simplical grid need less computer memory; the problem of the prohibitively large memory allocation required for the large number ( $>10^6$ ) of simplical cells is now eliminated – the new version can handle such cases even on the average desktop computers. In addition, generation of the Monte Carlo events, in case of large number of cells, may be even significantly faster.

To be submitted to Computer Physics Communications

keywords: Monte Carlo (MC) simulation and generation, particle physics, phase space.

IFJPAN-V-05-05 June 2005

<sup>\*</sup>Supported in part by EU grant MTKD-CT-2004-510126, in the partnership with CERN PH/TH Division

### 1 Introduction

FOAM program is designed to be an universal MC event generator/integrator. It can be used for generating weight one events and for evaluating integrals. FOAM employs combinations of two MC techniques: importance and stratified sampling known from older programs oriented for these tasks VEGAS [1] and MISER [2]. The most important and most sophisticated part of the FOAM algorithm is the procedure of dividing the integration region into a system of cells referred to as a "foam". The cells in "foam" can be hyperrectangles, simplices or Cartesian product of both. The process of the cellular splittings is driven by the user defined distribution function such that minimization of the ratio of the variance of the weight distribution to average weight (calculating integrals) or the ratio of maximum weight to the average weight (generating events) is achieved. For the detailed description of FOAM algorithm we refer the interested reader to Refs. [3, 4]

Until now FOAM has passed practical tests in some applications to high energy physics. We believe that foundations of the algorithm are well established and our current work concentrates on the updates of the program/algorithm toward better efficiency and functionality.

At present, development path of FOAM program goes in two directions. In the recent paper [5] we describe its new compact version — mFOAM — with simplified use due to integration with ROOT system [6] at the expense of slightly limited functionality. In mFOAM only hyperrectangular foam is used. This seems to be sufficient for most probability distributions encountered in the every-day practice. However, in certain more advanced applications the simplical grid may be definitely a better solution. Hence, we do not abandon development of full version of FOAM, which is intended for an experienced user, in case when mFOAM fails.

In the previous version of FOAM simplical grid is encoded in the program in the straightforward way: all vertices of all simplices are stored directly in the computer memory. This may lead to problem for large number of cells  $N_c$  for large number of dimensions n, because amount of allocated memory grows roughly as a product of them,  $\sim n N_c$ . In a complex problems with millions cells and n > 10, the required amount of memory may exceed typical physical memory size on a modern typical desktop computers.

Let us note that this problem for the hyperrectangular foam was already solved in the FOAM development, by employing sophisticated way of encoding system of cells in the computer memory. With such a method, the memory consumption per hyperrectangle can be limited to a constant number per cell independent of n. The main idea from this method is extended here to a simplical grid. As a byproduct we shall get also a new faster and more stable method for computing volume of simplical cell, without the need of determinant evaluation.

In the presented new version 2.06 of FOAM, the are two main improvements: (i) the memory saving solution mentioned above, (ii) the introduction of the new abstract base class – TRND – which provides access to the library of three high quality random number generators. We do not follow in the development line of mFOAM of introducing ROOT's objects whenever possible, because FOAM is meant to be optionally used as a stand-alone

program, without ROOT. This is why we leave old organization of cells, with the integer indices instead of pointers<sup>1</sup>.

The paper is organized as follows: In Section 2 we discuss new memory saving solution for simplical grid. Next, in Section 3 we describe changes in the code and compare performance of old and new algorithms. Appendix covers some technical details relevant for efficient encoding of the foam of simplical cells.

# 2 Memory saving algorithms for simplices.

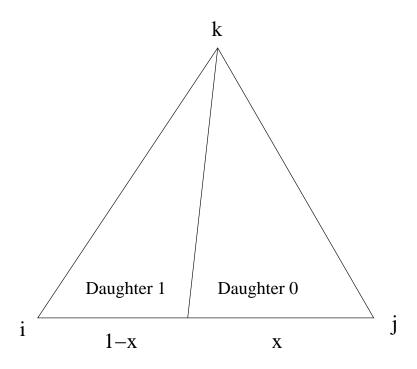


Figure 1: Split of a simplex.

In the algorithm (code) of FOAM simplices are organized as a linked tree structure. Each cell (except the single root cell being the entire space) has its parent cell. All cells: parent and daughter cells are kept in the computer memory<sup>2</sup>. Parent cells, which underwent division, we call "inactive cells" and the remaining are called "active" ones. Each parent (inactive) cell has two daughters, active or inactive. The foam of cells is built during the exploration phase in the process of a binary split of cells. Fig. 1 visualizes schematically the split of n-dimensional simplex. In the figure we show vertices, edges and division plane (line) on the 2-dimensional plane spanned by the line of the "division edge", which

<sup>&</sup>lt;sup>1</sup>This may look artificial; the reason for that is to ensure persistency, when working with ROOT.

<sup>&</sup>lt;sup>2</sup>That costs factor 2 overhead in the memory consumption.

joins vertices i and j, and the other vertex k, which can be any of the remaining vertices,  $k \neq i$ ,  $k \neq j$ . The central line marks the intersection of our plane with the division plane between two daughter cells.

Let us denote by  $\vec{V}_i$  the Cartesian absolute coordinates of *i*-th vertex in the universal reference frame of the root cell. In the FOAM algorithm, after the cell division a new vertex  $V_{new}$  is put somewhere on the division edge (i, j) of the simplex

$$\vec{V}_{new} = x\vec{V}_i + (1-x)\vec{V}_j.$$
 (1)

The geometry of the division is defined unambiguously by specifying the division edge (two integers) and the division parameter x (one number of double type).

In the original FOAM absolute positions of all vertices  $\vec{V}_i$  are recorded in the computer memory as a list of Cartesian vectors defined in a universal reference frame tied up to the root cell. The above vector algebra is done in terms of such vectors, all in the same universal reference frame. (This is why memory consumptions grows with the dimension.)

On the other hand, during the MC exploration of each cell, one generates randomly MC points with the uniform distribution within any given cell using another kind of the internal coordinates<sup>3</sup> specific for a given simplex cell, which cannot be used for any other cell than this one. There is, however, very important exception from the above restriction: we may establish connection between the internal variables of the parent cell and the two daughter cells! This opens the way of eliminating the need of storing Cartesian vectors of all vertices  $\vec{V}_i$ , and thus reducing the memory consumption.

The basic idea is to look up recursively the linked tree of ancestors, starting from a given active cell and finishing with the root cell. In a single step upward one translates the internal coordinates of the daughter cell into internal coordinates of the parent cell. In the end the internal coordinates of any point in any active cell gets translated into the internal coordinates of the root cell, which are universal! In this way, we only need to know the n+1 Cartesian vectors of the vertices of the root cell, in order to translate every point in every active cell to an universal Cartesian vector. The universal Cartesian vector is, of course, needed to evaluate the distribution function (which knows nothing about foam of cells and its internal coordinates), and is also used for other purposes by the external user of the FOAM object.

The above translation from the daughter to the parent internal variables is more complicated for the simplical cells than for hyperrectangular cells and we shall describe it in the following in more details.

The essential point in the proper connecting of the internal coordinates of the parent and daughter cell is the careful choice of the origin point of the coordinate system of the internal variables in the relevant cells. The definition of the internal coordinates always distinguishes one of the vertices of a given cell<sup>4</sup>. Let us call this vertex the *origin vertex*.

As already indicated in Fig. 1 the division point is located on the interval (i, j). Following notation in the figure, if daughter number 0 has the origin vertex being vertex

<sup>&</sup>lt;sup>3</sup>For the internal coordinates  $\lambda_i, i = 1, 2, \dots, n+1$  we keep convention that  $\lambda_i \in \langle 0, 1 \rangle$  and  $\sum \lambda_i \leq 1$ . Furthermore one of them is equal zero  $\lambda_k = 0$ . See also Appendix.

<sup>&</sup>lt;sup>4</sup>The one for which  $\lambda_k = 0$ .

j then the transformation of the internal coordinates between the daughter cell  $(\lambda_l)$  and the parent cell  $(\lambda'_l)$  is just the following dilatation of just one i-th coordinate

$$\lambda_{i}^{'} = x\lambda_{i}.\tag{2}$$

Similarly, for daughter number 1 and parent cell sharing the origin vertex i we shall have

$$\lambda_{j}^{'} = (1 - x)\lambda_{j}.\tag{3}$$

What to do in a typical situation when the parent and daughter cell do not share the origin vertex as described above? The solution is simple, change origin vertex to the vertex which fits the dilatation scheme outlined above. The resulting additional transformation of the internal coordinates is described in Appendix.

The entire algorithm of building the absolute Cartesian coordinates using information stored in the ancestry line of the active cell can be summarized as follows:

- (a) For a given current active cell look for its parent. If our cell is already the root cell then translate  $\lambda$ 's into Cartesian coordinates and *exit*, else go to point (b).
- (b) Check if the origin vertex is in convenient location and optionally redefine the origin vertex performing transformation of Eq. (11) in Appendix. Go to point (c).
- (c) Perform the transformation of Eq. (2) or (3). Replace the current cell by its parent cell and return to point (a).

From now on it is obvious that we do not need to know and store the Cartesian vectors for all vertices of the simplical cells. However, for establishing the proper total normalization of the FOAM integrand over each cell we also need to know the volume of the cell. In the original FOAM algorithm it was evaluated using determinant of the Cartesian vectors of the vertices. Of course, with some effort, using the transformations described above we could calculate Cartesian vectors of all n+1 vertices and plug them into determinant. Luckily, it is not necessary, because we have found an alternative very simple method of calculating the volume of the simplical cell in which the information in the ancestry line of a cell is used, similarly as in decoding of absolute coordinates described above. Again, climb up the linked tree toward the root cell and at each step we perform the transformation relating volume of the cell V and its parent V', which is very simple. Following notation of Fig. 1, for daughter number 0 the following rule applies

$$V = xV' \tag{4}$$

while for daughter number 1 we should apply

$$V = (1 - x)V'. (5)$$

The above method is fast and it also turns out to be more stable numerically than the usual method based on evaluation of the determinants, especially at large n.

## 3 Changes in code

In the following we shall summarize on the changes in the C++ source code which implement the new method of coding simplical cells and other changes.

### 3.1 TFOAM and TFCELL class

The algorithm described above for "in flight" decoding of the absolute coordinates of the MC points inside any cell (without the need of knowing the vertex positions) and algorithm for volume calculation are implemented as two additional methods in TFCELL class: sophisticated translator of coordinates: GetXSimp(TFVECT &, TFVECT & , int ) and volume cell calculator CalcVolume(void). The method GetXSimp is used in few places in program to provide argument for the distribution function and during event generation to translate internal coordinates of event to Cartesian coordinates, required by the user. The method CalcVolume calculates the volume of the cell. It replaced permanently the old method MakeVolume based on determinants.

The new solution with "in flight" transformation of coordinates is active in the default configuration. However, it might be sometimes convenient to switch back to the old algorithm. For instance it is required if one wants to use the plotting procedures: LaTexPlot2dim or RootPlot2dim. The same applies for certain debugging methods. To address these issues we have introduced in the TFOAM class a new switch m\_OptVert and corresponding setter method SetOptVert( int ). This switch has an analogous meaning to m\_OptMCell switch already introduced for hyperrectangles. In order to activate storing positions of vertices in the memory the user may invoke FoamX->SetOptVert(0), which resets m\_OptVert to 0 (the default value is 1) before the initialization of the FOAM object (MC generator).

$N_c$	$2.5 \times 10^{5}$	$5 \times 10^5$	$10^{6}$
OptVert=	0		
Mem (Mby)	143	211	346
CPU (min)	118	392	1453
OptVert=	1		
Mem (Mby)	116	156	243
CPU (min)	67	156	401

Table 1: Performance comparison of new and old algorithms.

In order to compare CPU and memory consumption in new and old algorithms we performed some tests for function Camel included in TFDISTR class. In each test we built grid consisting of a few hundred thousands to million 6-dimensional simplical cells and generate 200k events. For computations we used high-end PC equipped with AMD64 processor running with 2 GHz clock and 2 Gby RAM. In Tab. 1 we compare total virtual memory consumption, shown by top utility program and CPU time needed to complete each task.

The memory consumption is significantly lower for new algorithms. Moreover difference in memory consumption between old and new algorithms scales linearly, as expected, with the number of cells. For the finest grid studied reaches above 100 Mby  $^5$ . Obviously for the larger number  $N_c$  memory consumption in old algorithms quickly becomes critical: program with old algorithms can not be run at all while computations for new algorithms are still feasible. To see this barrier we repeated the last test with  $N_c = 10^6$  on older desktop computer with 500 Mby of RAM. We succeeded to complete it only with new algorithms. Program switched to old algorithms did not deliver the result even after a week probably due to heavy swap.

As we see, new algorithms are also significantly faster. At this moment we can not give detailed explanation to this rather surprising observation. Definitely some role can play fact that vertices in old algorithms are accessed in random pattern. Rarely used vertices have tendency to be moved outside the cache memory or if the foam has indeed many cells even outside physical RAM to swap disk. This results in many cache conflicts or even worser swapped vertices have to be read from disk. These operations introduce significant time overhead which can slow down the program progress more than additional modest computational effort in new algorithms.

From the above tests we conclude that our memory saving solution was worth an extra programming effort and indeed improved performance of FOAM with simplical cells.

## 3.2 TRND - collection of random number generators

The essential new auxiliary part of the FOAM package is a small library of the three random number generators inheriting from the pure Abstract Base Class (interface) TRND. In its construction we had the following very clear specification in mind:

- The library of the random number generators should be *extensible*, i.e. its user could easily add another random number generator with well defined minimum of functionality. This implies that all r.n.g. classes should inherit from certain relatively simple pure abstract base class (interface).
- The minimum functionality is defined as follows:
  - Possibility to set initial "seed" in form of just one integer.
  - Existence of a method to generate a single uniform random number.
  - Existence a method to generate a series of the uniform random numbers in a single call.
  - It should be easy to record status of random number generator and restart it using recorded data. This is, of course, assured by the persistency mechanism of ROOT.

<sup>&</sup>lt;sup>5</sup>In the same test repeated on SGI-2800 supercomputer we found even deeper reduction. However we are in serious doubt if the memory usage shown by the queue system is correct.

• The library of the random number generators should be *versatile* i.e. it should include at least one example of the generator, which features the best possible randomness (RANLUX), one which is fast and has extremely long series (Mersenne Twister), and possibly some legacy code, which has been widely used in the past (RANMAR). From these options user may easily choose something which fits his particular Monte Carlo project.

After reviewing the existing libraries of the r.n. generators we concluded that none of them<sup>6</sup> does meet the above specification, and we decided to create such a library of our own, with our own universal and minimalistic *interface*. The user of FOAM may easily add his own favorite r.n. generator to this collection.

Abstract Base Class TRND provides user interface to collection of the random numbers generators. It replaces the old class TPSEMAR of the original FOAM. At present, three random number generators are included: TRanmarEngine is an implementation of the well known RANMAR generator [7]. Class TRanmarEngine is practically identical with the old TPSEMAR class and both produce the same sequences of the MC events, if initialized with the same seed. We recommend it as a default one because it is fast and reliable.

RANLUX is the best of known available random number generators in the literature [8]. It is implemented here under the name TRanluxEngine, following closely ref. [9]. This generator has excellent spectral properties and user defined "luxury level". At the highest possible level=4 its 24 bits of mantissa are completely chaotic, however, already for default level=3 its quality is high enough for most of practical applications.

The third choice included in our small library of the random number generators is TRMersenneTwister - implementation of the recently developed Mersenne Twister random number generator, which is very fast and has huge period  $2^{19937} - 1$  [10]. As an example: the following line of code

TRND \*PseRan = new TRanmarEngine(); // Create random number generator

creates an instance of RANMAR generator with the default value of the so-called seed.

Most of the code and method names were adopted from CLHEP class of random numbers generators [11]. All generators are fully persistent; their state can be written into disk and restored later using persistency mechanism of ROOT.

The great profit from the persistency implementation is that the class objects (random number generators) restored from the disk do not need any reinitialization – they can be just used immediately to generate the next random number, following the one generated before the disk-write, as if there was no disk-write and disk-read at all!

<sup>&</sup>lt;sup>6</sup>The class TRandom in ROOT almost fulfills our specification. We want, however, that FOAM is able to work also in the stand-alone mode without ROOT. In addition TRandom has a lot of extra functionality which we do not need and it still does not include RANLUX.

## 4 Conclusions

FOAM package has reached the level of the mature MC tool to be used by the advanced builders of the MC event generators. In this work we implement certain technical improvements in the code, without any essential modification of the MC algorithm. The main change in the presented new version 2.06 is the new more efficient method of encoding the simplical foam of cells in the computer memory. The sophistication of the simplical foam is now upgraded to the same level as of the hyperrectangular one. In addition, we add a more sophisticated library of the random number generators with the universal interface. The other features of the package remains the same as in version 2.05.

# Acknowledgments

The work was partially supported by EU grant MTKD-CT-2004-510126, realized in the partnership with CERN PH/TH Division. We thank to ACK Cyfronet AGH Computer Center for granting us access to their PC clusters and supercomputers funded by the European Commission grant IST-2001-32243 and the Polish State Committee for Scientific Research grants: 620/E-77/SPB/5PR UE/DZ 224/2002-2004, 112/E-356/SPB/5PR UE/DZ 224/2002-2004, MNiI/SGI2800/IFJ/009/2004 and MNiI/HP\_K460-XP/IFJ/009/2004.

# References

- [1] G.P. Lepage, J. Comput. Phys. 27 (1978) 192.
- [2] W.H. Press and G.R. Farrar, Computers in Physics 4 (1990) 190, CFA-3010.
- [3] S. Jadach, Comput. Phys. Commun. 152 (2003) 55, physics/0203033.
- [4] S. Jadach, Comput. Phys. Commun. 130 (2000) 244, physics/9910004.
- [5] S. Jadach and P. Sawicki, physics/0506084.
- [6] R. Brun and F. Rademakers, Nucl. Inst. Meth. in Phys. Res. A389 (1997) 81, Proceedings AIHENP'96 Workshop, Lausanne, Sept. 1996, See also http://root.cern.ch/.
- [7] G. Marsaglia, B. Narasimhan and A. Zaman, Comput. Phys. Commun. 60 (1990) 345.
- [8] M. Luscher, Comput. Phys. Commun. 79 (1994) 100, hep-lat/9309020.
- [9] F. James, Comput. Phys. Commun. 79 (1994) 111.
- [10] M. Matsumoto and T. Nishimura, ACM Transactions on Modeling and Computer Simulation 8 (1998) 3.
- [11] CLHEP Project, http://wwwinfo.cern.ch/asd/lhc++/clhep.

## **Appendix**

A simplex in n dimension has n+1 vertices and each of them can be regarded as an origin point of coordinate system. The other n vertices define vector directions which span the vector space. More precisely, arbitrary vector  $\vec{P_i}$ , connecting i-th vertex with a certain point P can be written as

$$\vec{P}_i = \sum_k \lambda_k \vec{w}_k \quad (k \neq i) \tag{6}$$

in the internal basis of vectors  $\vec{w}_k = \vec{V}_k - \vec{V}_i$ , where  $\vec{V}_k$  is absolute position of k-th vertex. There are n internal coordinates because  $\vec{w}_i = 0$ . However, it is convenient to adopt convention that there are n+1 coordinates and  $\lambda_i = 0$ .

In our algorithm we shall use coordinates  $(\lambda_l)$  to parametrize position of points *inside* the simplex or eventually on its surface. This leads to additional conditions

$$\lambda_k \geq 0 \quad (k \neq i)$$

$$\sum_{k \neq i} \lambda_k \leq 1.$$

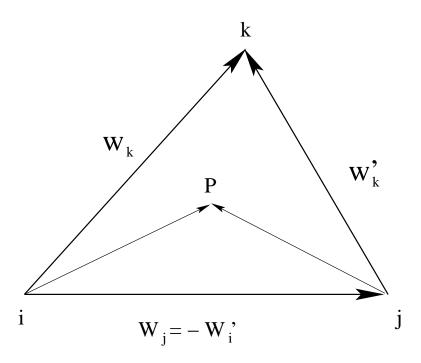


Figure 2: Transformation of internal coordinates under change of origin point.

An important component of our memory saving algorithm is transformation that changes the origin point of coordinate system from one vertex to another. In order to derive transformation law one has to relate coordinates of point P, residing inside the simplex, in the old and new basis (see Fig. 2). For the vector  $\vec{P}_i$  originating from i-th vertex we have

$$\vec{P}_i = \sum_{k \neq i} \lambda_k \vec{w}_k \tag{7}$$

and similarly for vector  $\vec{P_j}$  originating from j-th vertex

$$\vec{P}_j = \sum_{k \neq i} \lambda_k \vec{w}_k - \vec{w}_j. \tag{8}$$

Since  $\vec{w}_i' = -\vec{w}_j$  and  $\vec{w}_k = \vec{w}_k' - \vec{w}_i'$  we have further

$$\vec{P}_{j} = \sum_{k \neq i} \lambda_{k} (\vec{w}_{k}' - \vec{w}_{i}') + \vec{w}_{i}'. \tag{9}$$

Finally

$$\vec{P}_{j} = \sum_{k \neq i, k \neq j} \lambda_{k} \vec{w}_{k}' + (1 - \sum_{k \neq i} \lambda_{k}) \vec{w}_{i}'. \tag{10}$$

Coefficients before vectors  $\vec{w}'$  are now the new internal coordinates. The transformation law reads as follows

$$\lambda'_{k} = \lambda_{k} \quad (k \neq i, k \neq j)$$

$$\lambda'_{i} = 1 - \sum_{k \neq i} \lambda_{k}$$

$$\lambda'_{j} = 0.$$
(11)